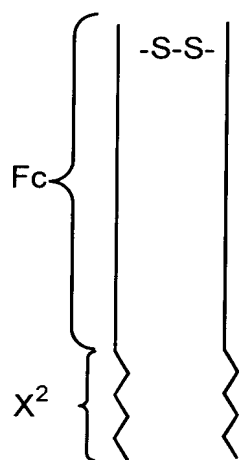
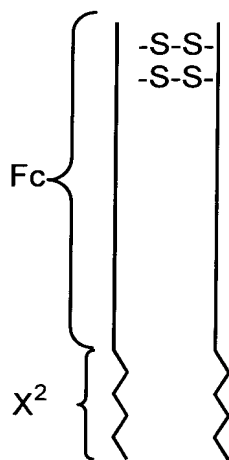
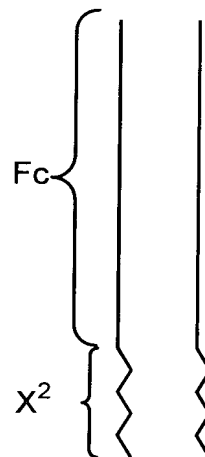


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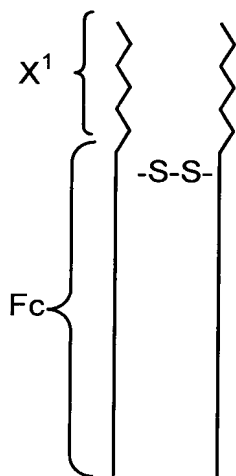
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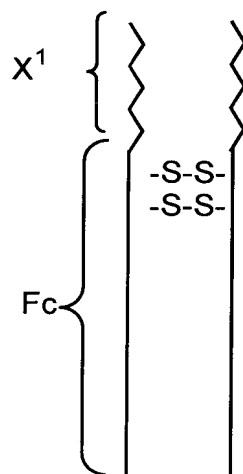
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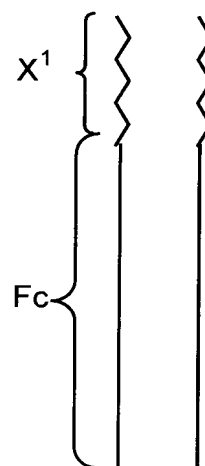
C



D



E



F

FIGURE 2

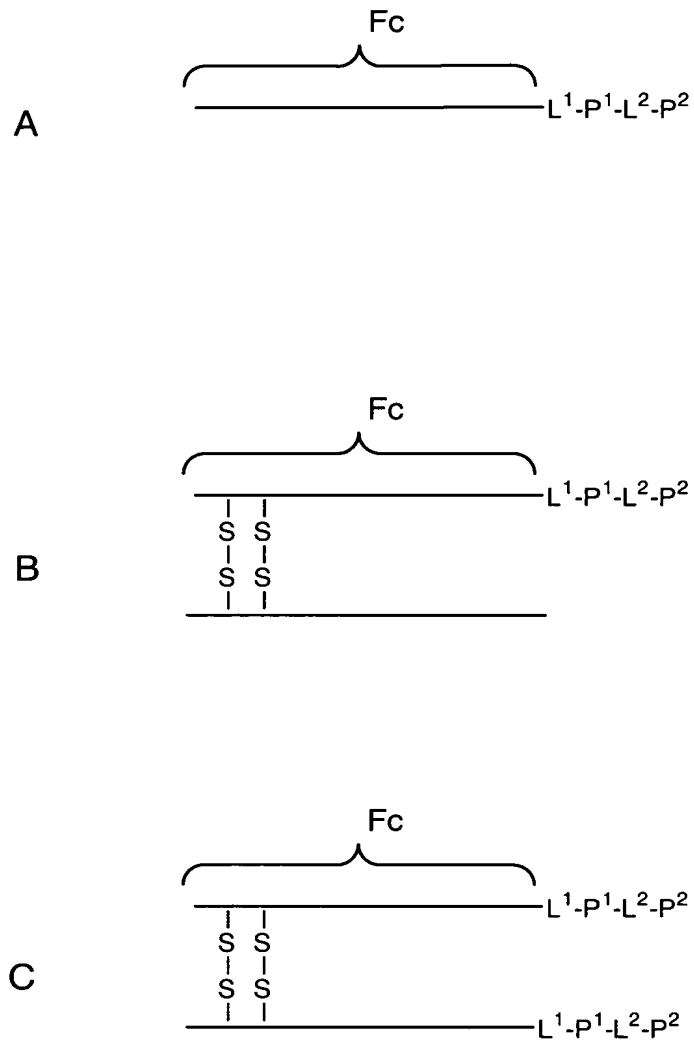


FIGURE 3A

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ATGGACAAAAC TCACACATGTCCACCTTGTCCAGCTCCGGAAC TCCTGGGGGGACCGTCA
1  -----+-----+-----+-----+-----+-----+-----+ 60
TACCTGTTTGTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCTGGCAGT

a   M D K T H T C P P C P A P E L L G G P S -

GTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC
61  -----+-----+-----+-----+-----+-----+-----+ 120
CAGAAGGAGAAGGGGGT TTTGGGTTCTGTGGGAGTACTAGAGGCCTGGGGACTCCAG

a   V F L F P P K P K D T L M I S R T P E V -

ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
121 -----+-----+-----+-----+-----+-----+-----+ 180
TGTACGCACCAACACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC

a   T C V V V D V S H E D P E V K F N W Y V -

GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAGC
181 -----+-----+-----+-----+-----+-----+-----+ 240
CTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGC

a   D G V E V H N A K T K P R E E Q Y N S T -

TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
241 -----+-----+-----+-----+-----+-----+-----+ 300
ATGGCACACCAAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATG

a   Y R V V S V L T V L H Q D W L N G K E Y -

AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAGCC
301 -----+-----+-----+-----+-----+-----+-----+ 360
TTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGG

a   K C K V S N K A L P A P I E K T I S K A -

AAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCATCCCGGGATGAGCTGACC
361 -----+-----+-----+-----+-----+-----+-----+ 420
TTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGG

a   K G Q P R E P Q V Y T L P P S R D E L T -

AAGAACCAGGTGACGCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG
421 -----+-----+-----+-----+-----+-----+-----+ 480
TTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCAC

a   K N Q V S L T C L V K G F Y P S D I A V -

GAGTGGGAGAGCAATGGGCAGCCGAGAACAAC TACAAGACCACGCCTCCCGTGTGAGAC
481 -----+-----+-----+-----+-----+-----+-----+ 540
CTCACCTCTCGTTACCCGTGGGCTCTTGTGTGATGTTCTGGTGCAGGAGGCACGACCTG

a   E W E S N G Q P E N N Y K T T P P V L D -

TCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
541 -----+-----+-----+-----+-----+-----+-----+ 600
AGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTC

a   S D G S F F L Y S K L T V D K S R W Q Q -

GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG
601 -----+-----+-----+-----+-----+-----+-----+ 660
CCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGTGTCGTCTTC

a   G N V F S C S V M H E A L H N H Y T Q K -

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